Directed Evolutio	n of Microorganisn
Schellenberger et	al.
SN# 10/037,677	
Docket No. GC56	0-D1
Sheet 1 of 10	•

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	GCGCACTATGAAGGCCACAAGATCATTGAGATTGGTGCCGTTGAAGTGGTGAACCGTCGCCTGACGGGCAATAAC 150	A H Y E G H K I I E I G A V E V N N R N L T G N N TICCATGITTATCICAAACCCGATGGCTGGTGGAAGCCTITGGCGTACATGGTATTGCCGATGAATTI 225		⋖		MDYIRGAELVI	CATAACGCAGCGTTCGATATCGGCTTTATGGACTACGAGTTTTCGTTGCTTAAGCGCGGATATTCCGAAGACCAAT 375	Z
	0990	T G CCGATG		AGTT(m L	CGAA	_
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-	GAA(N /15	>	TAT	Ш	-	IAAG	×
"	TGGT	V V	"	CTA	Ш	>	DCT	-
	A A G]	E CCTI	A 7	16GA	Ш	_	15	
-mutD	116	V AAG		TCA.			Ĕ	
1 T R O 1 V L D T	GTGCCGT1	G A	اخا	SAGT	-mutD-	D E F	AGT	- mutD-
-	. GGT	GAT	mutC	GAT	ΙĪ	۵	TAC	— mutī ∀ E
0	3AT1	1 36T6	>	3091	Ш	∢	GAC	۵
~	TGA	6C T C		AGT/		>	TAT	Σ
-	CAT	1 20	~	CGA	Ш	ш		ш
1 1	AGAT	,		1TGC	Ш	F A E v	550	9
	ACA	H K I I E AACCCGATCGGCTG	V Y L K P D R L V	CGT		<u>⊢</u>	ATA	D 1 G
ဟ	- S S	CTCA	$\parallel \parallel \perp$	V CC A	.	<u> </u>	TCG	LL
Σ	GAA	TAT(>	4AGC	Ш	×	3CGT	⋖
∀	TAT ;	> <u>1</u>	>	GAT/	Ш	٥	GCA	⋖
-	: GCAC	ECAT H	=	CTC	11,	<u> </u>	LAAC	z
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FIG._1A

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AAC/	z	333	∢	CAC	⊢	CAG		CAT	✓
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4AG(~	2	_	3GA(G	Ĕ	"	099	>
361/	G	TTA(SAAC	Шш	E	>	5	
3	F P G	3CA	∢	ATG(Σ	ij	>	000	ں
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ATG.	Σ	CAC	=	Ĕ	LL	TA		3GA/	9
AAA		CTG		SCT	<	AAG	×	360	9
AGG	- mutD	ACG	-mutD-	ATG	-mutD	AGT,	-mutD-	4AA(~
99	₽	CGA	11 "	100	S	GC A.	11 ~	AAG/	0 ×
GTG	>	AAA	×	ACG	⊢	CAG	0	CAG.	-mutD-
900	1	AGT	၂၂ တ	CAA	0	193	∝	3TG	>
13	S L	AAC	z	GGT	<u>ن</u>	GTA	>	CT G	
AGC	1	GAT	N 0 1	GGT	<u>ن</u>	ATT	> -	GAT	
GAT	V T D	ATA		ACC	-	29	~	213	R L D L
ACC	-	GAA	⊢	ATG	Σ	CAG	0	CGT	
GTC	>	TAC	>	900	∢	ATT	0 -	000	∢
AAG	~	25	∝	573	_	ACA	-	GAA	lω
161	ပ	GCT	∢	TAT	>	GCA	∢	CAT	±
ACTITCTGTAAGGTCACCGATAGCCTTGCGGTGGCGAGGAAAATGTTTCCCGGTAAGCGCAACAGCCTCGATGCG	14.	TTATGTGCTCGCTACGAAATAGATAACAGTAAACGAACGCTGCACGGGGCATTACTCGATGCCCAGATCCTTGCG	ں	GAAGTTTATCTGGCGATGACCGGTGGTCAAACGTCGATGGCTTTTGCGATGGAAGGAGAGACACAACAACAA	>	GGTGAAGCAACAATTCAGCGCATTGTACGTCAGGCAAGTAAGT	Ш	GCAGCTCATGAAGCCCGTCTCGATCTGGTGCAGAAGAAAGGCGGAAGTTGCCTCTGGCGAGCATAA 741	∢
ACT	-	TTA	_	GAA	Шш	GGT	<u>ن</u>	GCA	∢

			Sheet 3 of 1				0.110110	Motor : II	
	_		0_		3/10				_
	Eb_429T.dna Eb_GEBT.dna		Eb_429T.dna Eb_GEBT.dna		A A Eb_429T.dna A A Eb_GEBT.dna		Eb_429T.dna Eb_GEBT.dna		G C Eb_429T.dna G C Eb GEBT.dna
-09		120	AGCCCTGCTGGTGACC.	180	CGTGAAGCACCTGAAA	240	AGCCGAACCCGAAAGACACCAAC	300	GCGACATGATAATCACCGTCGC Eb_429Tdna
-20-	G T G A A C T T G T A A C T T	-11-	GGTAAAAA	170	GATCAGAC	230	GAGCCGAAGAGCCGAA	- 53 	TGCGACAT
40 +	GTTCCAAAT	100	3 C T G C T G G G G (160	0667667676	220	T C G A C G G G G T C G	280	TAAAGAGCAG
-30	TGATTATCT (-06	A G C G C T G C C A G C	150	CATTAAGA	210	GGTCATTT (270	0.000 P T C T T T C C C T P P P P C P C P C P
- 50-	ATCGTATGTT TATCGTATGTT	80	TTGTTGGCC	140	000000000000000000000000000000000000000	200	GGTATTGAGGT	560	ACGGCCT
-6-	ATGAGCT	-2-	GTTTCTG	130	GATAAGGG	190	900000	250	016010
	우 우		2 2		130		96 5		250

FIG._2/

310 370 370 370 430 490	310 66C6CAGCCC 66C6GCAGCCC 370 380 CTGTACAGCTA 430 430 444 AACCACGC AACAAAGTAAA ACCAAAGTAAA ACCAAAGTAAA	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	390 6 A C T G C G G T A A G G G T A T C G A A A C G C C C C G C G A A C C G C C C C		340 + 350 CATTGGTATTGCGGCC CATTGGTATTGCGGCC CACCAACCCGCTGCCG CACCAACCCGCTGCGCG CACCACTGCGTG CACCGCCACTGCGTG CACCGCCACTGCGTG CACCGCCACTGCGTG S20 S30 S20 S30	360 GCCACCCACCGGGTGAT GCCACCCACCGGGTGAT 420 CGCCCATTATTGCGGTC CGCCCATTATTGCGGTC CGCCCATTATTGCGGTC TGGCTGACTAACAAA GTGCTGACTAACAAA TCCGTCCCATTAACGAT	TGAT ED-4291.dna TGAT ED-6EBT.dna GGTC ED-4291.dna GGTC ED-4291.dna CAAA ED-4291.dna CAAA ED-4291.dna CGAT ED-4291.dna
	550	560	570	280	290	009	ı
550	1001000	CTGATGATCG	GCAAGCCGG	CGGGCTGACC	000000000000000000000000000000000000000	GGTATGGATGCCC	T G Eb_429T.dna T G Eb_GEBT.dna

FIG._21

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	610	620	- 0E9 	640	9 059	099		
610 610	ACCCACGC	CGGTAGAGGCCT	ATATCTCCAA ATATCTCCAA	A G A C G C C A A C C	CCGTTACCGA	TGCCTCTGCT	Eb_429T.dna Eb_GEBT.dna	
	029	089	069	002	7 0 7	720		
670 670	ATTCAGGCATTCAGGC	CATCAAACTGA	TTGCCACCAA	CTTGCGCCAGG	300010000	G G G G A C C A A C G G G G A C C A A C	Eb_429T.dna Eb_GEBT.dna	
	730	740	750	760	7,077	780		
730	CTCAAAGC	CCGTGAAACA	1660110001		CCGGGATGGC	CTTTAACAAC	Eb_429T.dna Eb_GEBT.dna	5/10
	790	800	810	820 1	830 -	840		
790	GCCAACCT	GGGCTATGTTC	A C G C C A T G G C	T C A C C A G C T G (GCGGCCTGTA	CGACATGGCC CGACATGGCC	Eb_429T.dna Eb_GEBT.dna	
	850	860	870	880 -	890	006		
820	CACGGGGT	GGCGAACGCGGT	TCCTGCTGCC	CCATGTCTGC	GCTATAACCT	GATTGCCAAC	Eb_429T.dna Eb_GEBT.dna	

FIG._20

	910	920	930	940;	950	096 -			
910 910	CCGGAAAA	ATTTGCCGATA ATTTGCCGATA	ATCGCCACCTTTATCGCCACCTTT	TATGGGGGAATATGGGGGAA	A A C A C C A C C G	GTCTTTCCACC GTCTTTCCACC	ACC Eb_429T.dna ACC Eb_GEBT.dna		
	970	086 -	066	1000	1010	1020			Scl SN Do
970 970	A T G G A C G C A	A G C G G A G C T G G A G C G G A G C T G G	GCCATCAGCGCC	CATTGCCCGT	CTGTCTAAAG	ATGTCGGGATC ATGTCGGGATC	Eb_429T.dna Eb_GEBT.dna		rected Evolute hellenberger 1# 10/037,67 ocket No. Go
	1030	1040	1050	1060	1070	1080		-	tion of N et al. 77 C560-D1
1030 1030	CCGCAGCA	CCTGCGTGAAC	CTGGGGGTAAA)	AGAGGCCGAC AGAGGCCGAC	CTTCCCGTACA:	TGGCAGAAATG TGGCAGAAATG	Eb_429T.dna Eb_GEBT.dna	6/10	Aicroorganis
	1090	1100	1110	1120	1130	1140			ms
1090	GCCCTGAA	C G G C A A C	G C C T C T C T A A C C C G C G C C T T C T C T A A C C C G C	A A C C C C C C C A A A A A C C C C C C	G G G A A C G A A A G G G G A A C G A A A	A A G A G A T T G C C A A G A G A T T G C C	Eb_429T.dna Eb_GEBT.dna		
	1150	1160	1170						-
1150 1150	GACATITIC	CCGCCAGGCAT	TTCTGA				Eb_429T.dna Eb_GEBT.dna		

FIG._2D

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

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	T.dna BT.dna	T.dna 3T.dna	T.dna 3T.dna	T.dna 3T.dna	- T.dna
	Eb_429T.dna Eb_GEBT.dna	Eb_429T.dna Eb_GEBT.dna	Eb_429T.dna Eb_GEBT.dna	Eb_429T.dna Eb_GEBT.dna	 A L Eb_429T.dna
100	QRCQLLGGKKALLVT QRCQLLGGKKALLVT	220 VVIFDGVEPNPKDIN VVIFDGVEPNPKDIN	340 SPEDCGKGIGIAATHPGD SPLDCGKGIGIAATHPGD	460 TASEVTRHCVLTNTK TASEVTRHCVLTNTK	580 KPAGLTAATGMD
-8-	F F G P G A V S V V G F F G P G A V S V V G	190 V K H L K A A G I E	310 IITVGG IITVGG	430 PIIAVNTTAG PIIAVNTTAG	SSO VSINDPLLMIG
40	M P D Y L V P N V N M P D Y L V P N V N	160 RAIKDGAVDQT RAIKDGAVDQT	280 ILAMPRKEQCDM ILAMPRKEQCDM	400 AGIETLTNPLP AGIETLTNPLP	520 PVIVSWRNLPS
-9-	M S Y R M S Y R	130 D K G L R A	V L D G I	370 LYSY LYSY	490 T K V K
	5 5	130	250 250	370 370	490

FIG._34

	Eb_429T.dna Eb_GEBT.dna		Eb_429T.dna Eb_GEBT.dna		Eb_429T.dna Eb_GEBT.dna		Eb_429T.dna Eb_GEBT.dna		Eb_429T.dna Eb_GEBT.dna
002	IATNLRQAVALGTN IATNLRQAVALGTN	820	HAMAHQLGGLYDMA HAMAHQLGGLYDMA	940	IATPMGENTTGLST IATPMGENTTGLST	1060	L G V K E A D F P Y M A E M L G V K E A D F P Y M A E M	!	ča ča
670	VTDASAIQAIKLIAT VTDASAIQAIKLIAT	790	G M A F N N A N L G Y V G M A F N N A N L G Y V	910	R Y N L I A N P E K F A D I R Y N L I A N P E K F A D I	1030	S K D V G I P Q H L R E S K D V G I P Q H L R E	1150	NEKEIADIFRQA NEKEIADIFRQA
610 640	THAVEAY ISKDANP THAVEAY ISKDANP	730 760	L K A R E N M A C A S L L A L K A R E N M A C A S L L A	850 880	H G V A N A V L L P H V C R H G V A N A V L L P H V C R	970 1000	M D A A B L A I S A I A R L M D A A B L A I S A I A R L	1090 1120	A L K D G N A F S N P R K G A L K D G N A F S N P R K G
_	610		730	ω	850 850	3,	970 970	-	1090

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

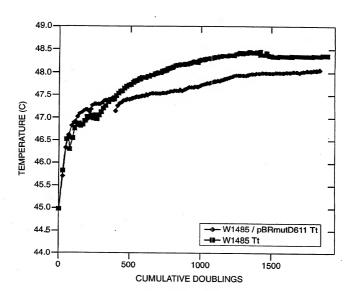


FIG._4

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